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Laboratoire de Chimie Bacterienne, Centre National de la Recherche Scientifique, Marseille, France.

The gene of high molecular weight, multiheme cytochrome c (Hmc) from the sulfate-reducing bacterium *Desulfovibrio vulgaris* Hildenborough has been overexpressed in *Desulfovibrio desulfuricans* G200. The recombinant protein has been purified. Its molecular weight (65,600), amino acid composition, and NH<sub>2</sub>-terminal sequence were found to be identical to those of the wild-type protein. The recombinant protein has been spectroscopically characterized (optical spectrum, EPR, circular dichroism) and compared to the wild-type protein. We have found 16 hemes per molecule by iron analysis and the pyridine hemochrome test. Both high- and low-spin features were observed in the EPR spectrum. A detailed spin quantitation analysis indicates 1 or 2 high-spin hemes and 14 or 15 low-spin hemes per molecule. The redox potentials of the hemes determined by voltammetric techniques gave an average of three different values, 0, -100, and -250 mV (versus NHE), for the wild-type and the recombinant cytochrome. The low potential values are similar to the values observed for the bis(histidiny) coordinated hemes of cytochrome c<sub>3</sub>. A comparison of the arrangement of heme binding sites and coordinated histidines in the amino acid sequences of cytochrome c<sub>3</sub> and Hmc has shown that the latter contains four domains, three of which are complete c<sub>3</sub>-like domains, while the fourth represents an incomplete c<sub>3</sub>-like domain which may contain His-Met coordinated hemes. These data are in agreement with the detailed study of the number and types of hemes reported in this paper.

PMID: 1313289 [PubMed - indexed for MEDLINE]

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